

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2004, 12:02:16 ; Search time 0.001 Seconds

(without alignments)  
2758.896 Million cell updates/sec

Title: us-10-626-445-5

Perfect score: 1176

Sequence: 1 atgcgcagctcacaagctac.....accagtcagctctctctga 1176

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 0.5

Searched: 1 segs, 1173 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : us-09-414-010-1:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# ALIGNMENTS

Result 1  
us-09-414-010-1

Query Match 58.8%; Score 691.101; DB 1; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 0;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

| Query | Score   | Match | Length | ID | Description     |
|-------|---------|-------|--------|----|-----------------|
| 1     | 691.101 | 58.8  | 1173   | 1  | us-09-414-010-1 |
| 2     | 16.8    | 1.4   | 1173   | 1  | us-09-414-010-1 |

|    |      |   |
|----|------|---|
| QY | 301  | TCGTCTACAAATATGTCCTTCATTAAGCTACGATGATACAGTCAAGTTCCTCAATGCTGTG 360 |
| DB | 301  | TCGTCTACAAATATGTCCTTCATTAAGCTACGATGATACAGTCAAGTTCCTCAATGCTGTG 360 |
| QY | 361  | TCCTATAGAGGCTCAACACACGTCGATCATGAAGATGTTGCTCAAAATGGTGGCTGTGG 420   |
| DB | 361  | TCCTATAGAGGCTCAACACACGTCGATCATGAAGATGTTGCTCAAAATGGTGGCTGTGG 420   |
| QY | 421  | ATACGCTCTTCTGTTAAATGCGCGATGATTCGGCTTCAGATTCTTGAAGAACAGC 480       |
| DB | 421  | ATACGCTCTTCTGTTAAATGCGCGATGATTCGGCTTCAGATTCTTGAAGAACAGC 480       |
| QY | 481  | ACGAACAAAGAGAGCTGAGCCGCTTGTATACAGAGGTGATACATCCGACATTAACA 540      |
| DB | 481  | ACGAACAAAGAGAGCTGAGCCGCTTGTATACAGAGGTGATACATCCGACATTAACA 540      |
| QY | 541  | ATGCTCTTGAATTCCTGCTTCCTGTCATCTCTGGCTTATTCATGATACAGATTAC 600       |
| DB | 541  | ATGCTCTTGAATTCCTGCTTCCTGTCATCTCTGGCTTATTCATGATACAGATTAC 600       |
| QY | 601  | TGAGAGCTGTGAAGAGCTGAGGCTCTCAGTAGAGTGCCCTAGCCATGCTGATTCCTCACT 660  |
| DB | 601  | TGAGAGCTGTGAAGAGCTGAGGCTCTCAGTAGAGTGCCCTAGCCATGCTGATTCCTCACT 660  |
| QY | 661  | ACTCTTTCAGTGTCTTCAAGACACTTACACAGAGCTGGGCTTGCAGAGCAAGTAAT 720      |
| DB | 661  | ACTCTTTCAGTGTCTTCAAGACACTTACACAGAGCTGGGCTTGCAGAGCAAGTAAT 720      |
| QY | 721  | CTGTGATTTGAAGAAATAGCTGATCTCGTCACTCAGAAAGTCCCTGAGAAAGAGCAGC 780    |
| DB | 721  | CTGTGATTTGAAGAAATAGCTGATCTCGTCACTCAGAAAGTCCCTGAGAAAGAGCAGC 780    |
| QY | 781  | ATCTGTGTCTTAAAGACTCAATGACAGAGATATCACTGCTTCAAAAGTGGCTTC 840        |
| DB | 781  | ATCTGTGTCTTAAAGACTCAATGACAGAGATATCACTGCTTCAAAAGTGGCTTC 840        |
| QY | 841  | TTCTGGCGATGGAAAGTGAAGGCTTGGCCAAAGGAGAGAGCAGAGCTTCCAGAGC 900       |
| DB | 841  | TTCTGGCGATGGAAAGTGAAGGCTTGGCCAAAGGAGAGAGCAGAGCTTCCAGAGC 900       |
| QY | 901  | AGGAAGCTAGCAGAGCTGAGGCTTCTGAGAGGCTTTGGCAATTTGCTGAGCTTCA 960       |
| DB | 901  | AGGAAGCTAGCAGAGCTGAGGCTTCTGAGAGGCTTTGGCAATTTGCTGAGCTTCA 960       |
| QY | 961  | TACTGTCTGTCAACATTTGCTTCACTTACCTTACCCAGAGAGGAGCCCAATGCTG 1020      |
| DB | 961  | TACTGTCTGTCAACATTTGCTTCACTTACCTTACCCAGAGAGGAGCCCAATGCTG 1020      |
| QY | 1021 | TGTAACAGATTCGCTTGGCTGCAATGATTCATTTGTTATATCCCTTCTGTAC 1080         |
| DB | 1021 | TGTAACAGATTCGCTTGGCTGCAATGATTCATTTGTTATATCCCTTCTGTAC 1080         |
| QY | 1081 | CCCTTGTGTCAACAGGCTTCCAGAGGCTTTCGAGAGTACTTGTGTGACAAAGCAA 1140      |
| DB | 1081 | CCCTTGTGTCAACAGGCTTCCAGAGGCTTTCGAGAGTACTTGTGTGACAAAGCAA 1140      |
| QY | 1141 | CGAGGCTGTCAAGAAC---CAGTCAGATCTTTCTTGA 1176                        |
| DB | 1141 | CGAGGCTGTCAAGAAC---CAGTCAGATCTTTCTTGA 1176                        |

RESULT 2  
us-09-414-010-1/c

Query Match 1.4%; Score 16.8; DB 1; Length 1173;  
Best Local Similarity 61.4%; Pred. No. 0;  
Matches 27; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

|    |     |   |
|----|-----|---|
| QY | 872 | AAAGGAGTACAGAGCTTCTCAGAGGAGAGCTAGAGCAGG 915 |
| DB | 872 | AAAGGAGTACAGAGCTTCTCAGAGGAGAGCTAGAGCAGG 915 |
| QY | 915 | AAAGGAGTACAGAGCTTCTCAGAGGAGAGCTAGAGCAGG 915 |
| DB | 915 | AAAGGAGTACAGAGCTTCTCAGAGGAGAGCTAGAGCAGG 915 |

Mon Oct 25 12:02:36 2004

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Search completed: October 25, 2004, 12:02:18  
Job time : 1 secs